

ONLINE SEARCH REQUEST FORM

***** Keith C. Furman ***** 671500, 300 *****

USER _____ SERIAL NUMBER _____
ART UNIT 1814 PHONE 306-3453 DATE 1/21/93

Please give a detailed statement of requirements. Describe as specifically as possible the subject matter to be searched. Define any terms that may have special meaning. Give examples or citations, authors, or keywords, if known.

You may include a copy of the broadest and or relevant claim(s).

~~SEQ 10 NO: 13~~ ¹⁴

Please search the ~~highlighted portions~~ of the attached amino acid

sequence against protein data bases including GeneSeq. ~~Reverse translate the~~

~~highlighted portions and~~ ^{SEQ 10 NO: 13} Search against nucleic acid data bases including

GeneSeq.

DO NOT PRINT THE SEARCHES, but save ALL to a SINGLE COMBINED file on the attached diskette.

Thank you.

-1-

SEQ 13.ies
SEQ 14.ies

1-161

STAFF USE ONLY

COMPLETED 1/21
SEARCHER INWIL X4058
ONLINE TIME 36 TOTAL TIME 47
(in minutes)
NO. OF DATABASES _____

SYSTEMS
____ CAS ONLINE
____ DARC/QUESTEL
____ DIALOG
____ SDC
☒ OTHER CC

BEST AVAILABLE COPY

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-07-800-364a-13.res made by maryh on Thu 21 Jan 93
19:51:42-PST.

Query sequence being compared:US-07-800-364A-13 (1-1003)
Number of sequences searched: 131368
Number of scores above cutoff: 4260

Results of the initial comparison of US-07-800-364A-13 (1-1003) with:
Data bank : EMBL-NEW 12, all entries
Data bank : GenBank 74, all entries
Data bank : GenBank-NEW 12, all entries
Data bank : N-GeneSeq 9, all entries
Data bank : UEMBL 33_74, all entries

4. US-07-800-364A-13 (1-1003)

HUMOP1 Human OP-1 mRNA for osteogenic protein

LOCUS HUMOP1 1878 bp ss-mRNA PRI 29-MAY-1991
DEFINITION Human OP-1 mRNA for osteogenic protein
ACCESSION X51801
KEYWORDS OP-1 gene; osteogenic protein.
SOURCE Homo sapiens RNA.
ORGANISM Homo sapiens
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
REFERENCE 1 (bases 1 to 1878)
AUTHORS Oppermann,H.
JOURNAL Unpublished (1990)
STANDARD full automatic
REFERENCE 2 (bases 1 to 1878)
AUTHORS Oezkaynak,E., Rueger,D.C., Drier,E.A., Corbett,C., Ridge,R.J.,
Sampath,T.K. and Oppermann,H.
TITLE OP-1 cDNA encodes an osteogenic protein in the TGF-beta family
JOURNAL EMBO J. 9, 2085-2093 (1990)
STANDARD full automatic
COMMENT *source: tissue=placenta;
From EMBL entry HSOP1; dated 12-SEP-1990.
FEATURES Location/Qualifiers
polyA_signal 1850..1855
/gene="BMP3"
polyA_signal 1862..1867

```

        /gene="BMP3"
polyA_site      1878
                /gene="BMP3"
CDS             123..1418
                /gene="BMP3"
                /note="pre-propolypeptide; (AA -29 to 402)"
                /codon_start=1

/translation="MHVRSRLRAAPHSFVALWAPLFLLRSALADFSLDNEVHSSF IHR
RLRSQERREMQREILSILGLPHRPRPHLQGKHNSAPMFMLDLYNAMAVEEGGGPGGQG
FSYPYKAVFSTQGPPLASLQDSHFLTDADMVMSFVNLVEHDKEFFHPRYHHREFRDL
SKIPEGEAVTAAEFRIYKDYIRERFDNETFRISVYQVLQEHLGRESDFLLDSRTLWA
SEEGWL VFDITATSNHWVVNPRHNLGLQLSVETLDGQ SINPKLAGLIGRHGPQNKQPF
MVAFFKATEVHFRSIRSTGSKQRSQNRSKTPKNQEALRMANVAENSSSDQRQACKKHE
LYVSFRDLGWQDWIIAPEGYAAYYCEGECAPFLNSYMNATNHAIVQTLVHF INPETVP
        KPCCAPTQLNAISVLYFDDSSNVILKKYRNMVVVRACGCH"
CDS             123..206
                /gene="BMP3"
                /partial
                /note="signal peptide; (AA -29 to -1)"
                /codon_start=1
                /translation="MHVRSRLRAAPHSFVALWAPLFLLRSAL"
CDS             210..1034
                /gene="BMP3"
                /partial
                /note="propeptide; (AA 1-276)"
                /codon_start=1

/translation="DFSLDNEVHSSF IHRRLRSQERREMQREILSILGLPHRPRPHLQ
GKHNSAPMFMLDLYNAMAVEEGGGPGGQGF SYPYKAVFSTQGPPLASLQDSHFLTDAD
MVMSFVNLVEHDKEFFHPRYHHREFRDLSKIPEGEAVTAAEFRIYKDYIRERFDNET
FRISVYQVLQEHLGRESDFLLDSRTLWASEEGWL VFDITATSNHWVVNPRHNLGLQL
SVETLDGQ SINPKLAGLIGRHGPQNKQPFMVAFFKATEVHFRSIRSTGSKQRSQNR"
CDS             210..1017
                /gene="BMP3"
                /partial
                /note="propeptide; (alt.) (AA 1-270)"
                /codon_start=1

/translation="DFSLDNEVHSSF IHRRLRSQERREMQREILSILGLPHRPRPHLQ

```

GKHNSAPMFMLDLYNAMAVEEGGGPGGQGFSSYPYKAVFSTQGPPLASLQDSHFLTDAD

MVMSFVNLEHDKEFFHPRYHHREFRDLSKIPEGEAVTAAEFRIYKDYIRERFDNET

FRISVYQVLQEHLGRESDLFLLDSRTLWASEEGWLVDITATSNHWVVNPRHNLGLQL

```
CDS          SVETLDGQSINPKLAGLIGRHGPQNKQPFMVAFKATEVHFRSIRSTGSKQ"
              1021..1415
              /gene="BMP3"
              /partial
              /note="mature osteogenic protein; (AA 271-402)"
              /codon_start=3
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/translation="QNRSKTPKNQEALRMANVAENSSSDQRQACKKHELYVSFRDLGW

QDWIIAPEGYAAYYCEGECAFLNSYMNATNHAIVQTLVHFINPETVPKPCCAPTQLN

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CDS          AISVLYFDDSSNVILKKYRNMVVRACGCH"
              1038..1418
              /gene="BMP3"
              /partial
              /note="mature osteogenic protein; (AA 277-402)"
              /codon_start=1
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/translation="TPKNQEALRMANVAENSSSDQRQACKKHELYVSFRDLGWQDWII

APEGYAAYYCEGECAFLNSYMNATNHAIVQTLVHFINPETVPKPCCAPTQLNAISVL

```
YFDDSSNVILKKYRNMVVRACGCH"
BASE COUNT   411 a    592 c    541 g    334 t
ORIGIN
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Initial Score = 513 Optimized Score = 630 Significance = 30.73
Residue Identity = 64% Matches = 670 Mismatches = 303
Gaps = 59 Conservative Substitutions = 0

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      X      10      20      30      40      50      60
      GAATTCCG--AGCCCCATTGGAAGGAGTTCCGCTTTGACCTGACCCAGATCCCAGGCTGGGGG
      |      ||      |||||      |||||      |||||      |||||      |||||
GGAATTCTTCCACCCACGCTACCACCATCG--AG-AGTTCCGGTTTGATCTTTCAAGATCCCAGAAGGGGA
560  X  570      580      590      600      610      620

      70      80      90      100      110      120
GGCGGTCACAGCTGCGGAGTTCCGGATTTACAAGGTGCCCAGCATCC----AC-CTGC-TCAACAGGACCT
|| ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AGCTGTCACGGCAGCCGAATTCCGGATCTACAAG--GACTA-CATCCGGGAACGCTTCGACAATGAGACGTT
630      640      650      660      670      680      690

      130      140      150      160      170      180      190
CCACGTCAGCATGTTCCAGGTGGTCCAGGAGCAGTCCAACAGGGAGTCTGACTTGTTCTTTTGGATCTTCA
|| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CCGGATCAGCGTTTATCAGGTGCTCCAGGAGCACTTGGGCAGGGAATCGGATCTCTTCTGCTCGACAGCCG
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760          770          780          790          800          810          820          830
GAGCGCCACCTCTGTGCTCTACTATGACAGCAGCAACAACGTCATCCTGCGCAAGCACC GCAACATGGTGGT
|  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CAATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGTCATCCTGAAGAAATACAGAAACATGGTGGT
1330          1340          1350          1360          1370          1380          1390

          840          850          860          870          880          890          900
CAAGGCCCTGCGGCTGCCACTGAGTCAGCC---CGCCAGCCCTACTGCAGCCACCCTTCTCATCTGGATCGG
|  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CCGGGCCCTGTGGCTGCCACTAGCTCCTCCGAGAATTCAGACCCTTTGGGGCCAAGTTT---TTCTGGATCCT
1400          1410          1420          1430          1440          1450          1460

          910          920          930          940          950          960          970
GCCCTGCAGAGGCAGAAAACCCTTAAATGCTGTACAGCTCAGCAGGAGTGTGAGGGGCCCTCACTCTCGG
|  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CCATTGC---TCGCCCTTGGCCAGGAACCAGCAGAC-CAACTGCCTTTTGTGAGAC-CTTCCCTCCCTATCCC
1470          1480          1490          1500          1510          1520          1530

          980          990          1000  X
TGCCTACTT---CCTGTCAGGCTTCTGGGAATTC
|  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CAACT--TTAAGGTGTGAGAGTATTAGGAACATGAGCAGCAT
1540          1550          1560  X 1570

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/translation="MHVRSRLAAAPHSFVALWAPLFLLRSALADFSLDNEVHSSF IHR
RLRSQERREMQREILSILGLPHRPRPHLQGKHNSAPMFMLDLYNAMAVEEGGGP'GGQG
FSYPYKAVFSTQGPPLASLQDSHFLT DADMVMSFVNLVEHDKEFFHPRYHHREFRFDL
SKIPEGEAVTAAEFRIYKDYIRERFDNETFRISVYQVLQEHLGRESDLFL LDSRTLWA
SEEGWL VFDITATSNHWVVNPRHNLGLQLSVETLDGQSINPKLAGLIGRHGPQNKQPF
MVAFFKATEVHFIRSIRSTGSKQRSQNRSKTPKNQEAL RMANVAENSSSDQRQACKKHE
LYVSFRDLGWQDWIIAPEGYAAYYCEGECAFLNSYMNATNHAIVQTLVHF INPETVP
KPCCAPTQLNAISVLYFDDSSNVILKKYRNMVVRACGCH"

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BASE COUNT      285 a      490 c      422 g      251 t
ORIGIN

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Initial Score      =      496   Optimized Score      =      597   Significance = 29.65
Residue Identity   =      67%   Matches              =      630   Mismatches   = 255
Gaps               =          50   Conservative Substitutions      =          0

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          X          10          20          30          40          50          60
          GAATTCCG--AGCCCCATTGGAAGGAGTTCCGCTTTGACCTGACCCAGATCCCGGCTGGGGA
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
GGAATTCTTCCACCCACGCTACCACCATCG--AG-AGTTCCGGTTTGATCTTTCAAGATCCAGAAGGGGA
530      540      550      560      570      580      590

          70          80          90          100          110          120
GGCGGTACAGCTGCGGAGTTCCGGATTTACAAGGTGCCAGCATCC----AC-CTGC-TCAACAGGACCTT
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
AGCTGTACGGCAGCCGAATTCCGGATCTACAAG--GACTA-CATCCGGGAACGCTTCGACAATGAGACGTT
600      610      620      630      640      650      660

          130          140          150          160          170          180          190
CCACGTACGATGTTCCAGGTGGTCCAGGAGCAGTCCAACAGGGAGTCTGACTTGTTCTTTTGGATCTTCA
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
CCGGATCAGCGTTTATCAGGTGCTCCAGGAGCACTTGGGCAGGGAATCGGATCTCTTCTGCTCGACAGCCG
670      680      690      700      710      720      730

200      210      220      230      240      250      260      270
GACGCTCCGAGCTGGAGACGAGGGCTGGCTGGTGCTGGATGTACAGCAGCCAGTGACTGCTGGTTGCTGAA
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
TACCTCTGGGCCTCGGAGGAGGGCTGGCTGGTGTGATGATCACAGCCACCAGCAACCACTGGGTGGTCAA
740      750      760      770      780      790      800

          280          290          300          310          320          330
---GCGTCACAAGGACCTGGGACTCCGCCTCTATGTGGAGACTGAGGATGGGCACAGCGTGATCCTGGCCT
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
TCCGCGGCACA---ACCTGGGCCTGCAGCTCTCGGTGGAGACGCTGGATGGGCAGAGCATCAACCCCAAGTT

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          910
GCCCTGCAGAGGCAGAAAA
  |  | |
CCATTGCTC
1440      X

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8. US-07-800-364A-13 (1-1003)

MUSOP1G Mouse OP-1 mRNA for osteogenic protein 1

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LOCUS      MUSOP1G      1872 bp ss-mRNA      ROD      10-OCT-1991
DEFINITION Mouse OP-1 mRNA for osteogenic protein 1
ACCESSION  X56906
KEYWORDS   OP-1 gene; osteogenic protein.
SOURCE     Mus musculus RNA.
ORGANISM   Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE  1 (bases 1 to 1872)
AUTHORS    Ozkaynak, E., Schnegelsberg, P.N. and Oppermann, H.
TITLE      Murine osteogenic protein (OP-1): High levels of mRNA in kidney
JOURNAL    Biochem. Biophys. Res. Commun. 179, 116-123 (1991)
STANDARD   full automatic
COMMENT     Sequenced molecule was a DNA/cDNA composite:- genomic clone bases
            1-465, cDNA clone bases 267-1872.
            From EMBL entry MMOP1G; dated 26-SEP-1991.
FEATURES   Location/Qualifiers
            sig_peptide      104..190
                               /codon_start=1
            mat_peptide      977..1393
                               /product="osteogenic protein 1"
                               /gene="OP-1"
                               /codon_start=1
            CDS               104..1396
                               /gene="OP-1"
                               /product="pre-propeptide"
                               /codon_start=1

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/translation="MHVRSRLRAAPHFSFVALWAPLFLLRSALADFSLDNEVHSSF IHR
RLRSQERREMQREILSILGLPHRPRPHLQGKHNSAPMFMLDLYNAMAVEESGPDGQGF
SYPYKAVFSTQGPPLASLQDSHFLTADVMVSFVNLVEHDKEFFHPRYHHREFRFDLS
KIPEGERVTAAEFRIYKDYIRERFDNETFQITVYQVLQEHSGRESDFLLDSRTIWAS
EEGWLVDITATSNHWVVNPRHNLGLQLSVETLDGQSINPKLAGLIGRHGPNQKQPFM
VAFFKATEVHLRSIRSTGGKQRSQNRSKTPKNQEALRMASVAENSSSDQRQACKKHEL

```

YVSFRDLGWQDWIIAPEGYAAYYCEGECAPFLNSYMNATNHAIVQTLVHFINPDTVPK
PCCAPTQLNAISVLYFDDSSNVILKKYRNMVVRACGCH"

BASE COUNT 433 a 591 c 501 g 347 t
ORIGIN

Initial Score = 489 Optimized Score = 637 Significance = 29.20
Residue Identity = 65% Matches = 676 Mismatches = 300
Gaps = 55 Conservative Substitutions = 0

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      X      10      20      30      40      50      60
      GAATTCG--AGCCCCATTGGAAGGAGTTCCGCTTTGACCTGACCCAGATCCCGGCTGGGGA
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
AGAATTCTTCCACCCTCGATACCACCATCG---GGAGTTCCGGTTTGATCTTTCCAAGATCCCGAGGGCGA
    540 X    550      560      570      580      590      600

      70      80      90      100     110     120
      GCGGGTCACAGCTGCGGAGTTCCGGATTTACAAGG--TGC--CCAGCATCCACCTGCTCAACAGGACCTCC
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
ACGGGTGACCGCAGCCGAATTCAGGATCTATAAGGACTACATCCGGGAGCGATTTG-ACAACGAGACCTTCC
    610      620      630      640      650      660      670

130      140      150      160      170      180      190      200
      ACGTCAGCATGTTCCAGGTGGTCCAGGAGCAGTCCAACAGGGAGTCTGACTTGTTCTTTTGGATCTTCAGA
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
      AGATCACAGTCTATCAGGTGCTCCAGGAGCACTCAGGCAGGGAGTCCGACCTCTTCTTGCTGGACAGCCGCA
    680      690      700      710      720      730      740

      210     220     230     240     250     260     270
      CGCTCCGAGCTGGAGACGAGGGCTGGCTGGTGGTGGATGTACAGCAGCCAGTGACTGCTGGTTGCTGAAGC
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
      CCATCTGGGCTTCTGAGGAGGGCTGGTTGGTGGTTTGGATATCACAGCCACCAGCAACCACTGGGTGGTCAACC
    750      760      770      780      790      800      810

      280     290     300     310     320     330     340
      GTCACAAGGACCTGGGACTCCGCCTCTATGTGGAGACTGAGGATGGGCACAGCGTGGATCCTGGCCTGGCCG
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
      CTCGGCACAACCTGGGCTTACAGCTCTCTGTGGAGACCCTGGATGGGCAGAGCATCAACCCCAAGTTGGCAG
    820      830      840      850      860      870      880

      350     360     370     380     390     400     410
      GCCTGCTGGGTC--AACGGGCCCCACGCTCCCAACAGCCTTTTCGTGGTCACTTTCTTCAGGGCCAGTCCG-A
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
      GCCTGATTGGACGGCATGGACCCCA-GAAC-AAGCAACCCTTCATGGTGGCCTTCTTCAAGGCCA--CGGAA
    890      900      910      920      930      940      950

      420     430     440     450     460     470     480
      GTCC-CATCCGCACCCCTCGG-GCAGTGAGGGCCACTGAGGAGGAGGCAGCCGAGAGAAAGCAACGAGCTGCC
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
      GTCCATCTCCGTAGTATCCGGTCCACGGGGGGCA---AGCAG--CGCAGCC--AGAATCGCTCCAAGACGCC
    960      970      980      990     1000     1010     1020

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      490      500      510      520      530      540
GCAG-GCCAACCGACTCCCAGG--GATCTTTGATGACGTCCACGGCTCCACGGCC---GGCAGGTCTGCCG
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
AAAGAACCAAGAGGGCCCTGAGGATGGCCAGTGTGGCAGAAAACAGCAGCAGTGACCAGAGGCAGGCCTGCAA
      1030      1040      1050      1060      1070      1080      1090

550      560      570      580      590      600      610      620
TCGGCACGAGCTCTACGTACGCTTCCAGGACCTTGGCTGGCTGGACTGGGTTCATCGCCCCCAAGGCTACTC
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
GAAACATGAGCTGTACGTACGCTTCCGAGACCTTGGCTGGCAGGACTGGATCATTGCACCTGAAGGCTATGC
      1100      1110      1120      1130      1140      1150      1160

      630      640      650      660      670      680      690
AGCCTATTACTGTGAGGGGGAGTGCTCCTTCCCGCTGGACTCCTGCATGAACGCCACCAACCACGCCATCCT
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
TGCCTACTACTGTGAGGGAGAGTGCGCCTTCCCTCTGAACCTCTACATGAACGCCACCAACCACGCCATCGT
      1170      1180      1190      1200      1210      1220      1230

      700      710      720      730      740      750      760
GCAGTCCCTGGTGCACCTGATGAAGCCAAACGCAGTCCCCAAGGCGTGCTGTGCACCCACCAAGCTGAGCGC
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CCAGACACTGGTTCACTTCATCAACCCAGACACAGTACCCAAGCCCTGCTGTGCGCCACCCAGCTCAACGC
      1240      1250      1260      1270      1280      1290      1300

      770      780      790      800      810      820      830
CACCTCTGTGCTCTACTATGACAGCAGCAACAACGTATCCTGCGCAAGCACCGBAACATGGTGGTCAAGGC
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CATCTCTGTCTCTACTTCGACGACAGCTCTAATGTATCCTGAAGAAGTACAGAAACATGGTGGTCCGGGC
      1310      1320      1330      1340      1350      1360      1370      1380

      840      850      860      870      880      890      900
CTGCGGCTGCCACTGAGTCAGCCCG---CCGAGCCCTACTGC--AGCCAC-CCTTCTCATCTGGATCGGGCC
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CTGTGGCTGCCACTAGCTCTTCCTGAGACCCTGACCT-TTGGGGGGCCACACCTTTCCAAT-CTTCGATGT
      1390      1400      1410      1420      1430      1440      1450

      910      920      930      940      950      960      970
CTGCAGAGGCAGAAAACCCCTTAAATGCTGTACAGCTCAAGCAGGAGTGTACGGGGCCCTCACTCT-CGGTG
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CT-CACCATC-TAAGTCTCTCA----CTG-CCACCTTGGCGAGGA--GCCAACAGACCAACCTCTCCTGAG
      1460      1470      1480      1490      1500      1510

      980      990      1000 X
CCTACTTCCTGTC--AGGCTTCTGG--GAATTC
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CCTTC-CCCTACCTCCCCAACCGGAAGCATGTAGGGTTCCA
      1520      1530      1540 X 1550

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> O <
OI IO IntelliGenetics

> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-07-800-364a-14-pir.res made by maryh on Thu 21 Jan 93
19:33:50-PST.

Query sequence being compared:US-07-800-364A-14 (1-281)
Number of sequences searched: 44900
Number of scores above cutoff: 4198

Results of the initial comparison of US-07-800-364A-14 (1-281) with:
Data bank : PIR 34, all entries

	**** 53 standard deviations above mean ****					
1. S10529	*Osteogenic protein precursor	431	132	158	53.25	0
2. C39263	*Bone morphogenetic protein 7	431	132	158	53.25	0
	**** 51 standard deviations above mean ****					
3. JQ1184	Osteogenic protein 1 precurs	430	132	155	51.86	0
	**** 50 standard deviations above mean ****					
4. A39263	*Bone morphogenetic protein 5	454	111	153	50.93	0
5. A33925	*Vg-1-related protein precurs	438	128	152	50.47	0
6. B39263	*Bone morphogenetic protein 6	513	128	151	50.01	0
	**** 25 standard deviations above mean ****					
7. A41233	Bone morphogenetic protein ho	455	63	99	25.93	0
	**** 21 standard deviations above mean ****					
8. A26158	Decapentaplegic protein precu	588	54	89	21.30	0
	**** 19 standard deviations above mean ****					
9. C37278	Bone morphogenetic protein 2B	408	36	86	19.91	0
	**** 18 standard deviations above mean ****					
10. C39364	*GDF-1 embryonic growth facto	372	28	83	18.52	0
11. A29619	Vg1 embryonic growth factor -	360	55	82	18.06	0
	**** 17 standard deviations above mean ****					
12. B37278	Bone morphogenetic protein 2A	396	35	81	17.59	0
	**** 16 standard deviations above mean ****					
13. S16244	Bone morphogenetic protein 2	398	35	78	16.21	0
	**** 14 standard deviations above mean ****					
14. A30884	Inhibin beta-A chain precurs	426	20	74	14.35	0
15. B24248	Inhibin beta-A chain precurs	426	20	74	14.35	0
16. A39364	*GDF-1 embryonic growth facto	357	20	74	14.35	0
17. A35683	*GDF-1 embryonic growth facto	357	20	74	14.35	0
	**** 13 standard deviations above mean ****					
18. WFPGBA	Inhibin beta-A chain precurs	424	20	73	13.89	0
	**** 12 standard deviations above mean ****					
19. B40905	*Inhibin beta-A chain precurs	424	20	71	12.96	0
20. B40056	*Inhibin beta-A chain precurs	424	20	71	12.96	0

1. US-07-800-364A-14 (1-281)

S10529 *Osteogenic protein precursor - Human

ENTRY S10529 #Type Protein
 TITLE *Osteogenic protein precursor - Human
 DATE 15-Jun-1992 #Sequence 15-Jun-1992 #Text 15-Jun-1992
 PLACEMENT 0.0 0.0 0.0 0.0 0.0
 COMMENT *This entry is not verified.
 SOURCE Homo sapiens #Common-name man
 REFERENCE

#Authors Ozekaynak E., Rueger D.C., Drier E.A., Corbett C.,
 Ridge R.J., Sampath T.K., Oppermann H.

#Journal EMBO J. (1990) 9:2085-2093

#Title OP-1 cDNA encodes an osteogenic protein in the
 TGF-beta family.

#Reference-number S10529

#Accession S10529

#Cross-reference EMBL:X51801

SUMMARY #Molecular-weight 49313 #Length 431 #Checksum 128

SEQUENCE

Initial Score = 132 Optimized Score = 158 Significance = 53.25
 Residue Identity = 56% Matches = 161 Mismatches = 115
 Gaps = 11 Conservative Substitutions = 0

```

      X      10      20      30      40      50      60
      EPHWKEFRFDLTQIPAGEAVTAAEFRIYK-VPSIHLNRTLHVSMFQVVQEQSNRESDLFFL
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
140  VEHDKEFFHPRYHHREFRDLSKIPEGEAVTAAEFRIYKDYIRERFDNETFRISVYQVLQEHLGRESDLFLL
      150      160      170      180      190      200      210

      70      80      90      100     110     120     130
      DLQTLRAGDEGWLVLVDVTAASDCWLLKRHKDLGLRLYVETEDGHSVDPGLAGLLGQRAPRSQQPFVVTFFRA
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      DSRTLWASEEGWL VFDITATSNHWVVNPRHNLGLQLSVETLDGQSINPKLAGLIGRHGPQNKQPFMVAFFKA
      220      230      240      250      260      270      280

      140      150      160      170      180      190      200
      SPSPIRTFRAVRPLRRRQ-----PKKSNELPQANRLPGIFDDVHGSHGRQVCRRHELYVVSFQDLGWLDWVIA
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      TEVHFRSIRSTGSKQRSQNRSKTPKNQDEALRMAN-----VAENSSSDQRQACKKHELYVVSFRDLGWQDWIIA
      290      300      310      320      330      340      350

      210      220      230      240      250      260      270
      PQGYSAYYCEGECSFPLDSMNATNHAILQSLVHLMKPNVAVPKACCAPTKLSATSVLYYDSSNNVILRKHRN
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      PEGYAAYYCEGECAFLNSYMNATNHAI VQTLVHFINPETVPKPCCAPTQLNAISVLVYFDSSNVILKKYRN
      360      370      380      390      400      410      420

```

X

MVVKACGCH
 III IIIII
 MVVRACGCH
 430

2. US-07-800-364A-14 (1-281)

C39263 *Bone morphogenetic protein 7 - Human

ENTRY C39263 #Type Protein
 TITLE *Bone morphogenetic protein 7 - Human
 DATE 04-Oct-1991 #Sequence 04-Oct-1991 #Text 04-Oct-1991
 PLACEMENT 0.0 0.0 0.0 0.0 0.0
 COMMENT *This entry is not verified.
 SOURCE Homo sapiens #Common-name man
 REFERENCE
 #Authors Celeste A.J., Iannazzi J.A., Taylor R.C., Hewick
 R.M., Rosen V., Wang E.A., Wozney J.M.
 #Journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:9843-9847
 #Title Identification of transforming growth factor beta
 family members present in bone-inductive protein
 purified from bovine bone.
 #Reference-number A39263
 #Accession C39263
 #Cross-reference GB:M38695
 SUMMARY #Molecular-weight 49313 #Length 431 #Checksum 128
 SEQUENCE

Initial Score = 132 Optimized Score = 158 Significance = 53.25
 Residue Identity = 56% Matches = 161 Mismatches = 115
 Gaps = 11 Conservative Substitutions = 0

```

      X      10      20      30      40      50      60
      EPHWKEFRDLTQIPAGEAVTAAEFRIYK-VPSIHLNRTLHVSMFQVVQEQSNRESDLFFL
      |  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
140  VEHDKEFFHPRYHHREFRDLSKIPEGEAVTAAEFRIYKDYIRERFDNETFRISVYQVLQEHLGRESDLFL
      150      160      170      180      190      200      210

      70      80      90      100     110     120     130
      DLQTLRAGDEGWLVLDTAASDCWLLKRHKDLGLRLYVETEDGHSVDFGLAGLLGQRAPRSQQPFVVTFFRA
      |  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      DSRTLWASEEGWLVDITATSNHWVVNPRHNLGLQLSVETLDGQSINPKLAGLIGRHGPQNKQPFMVAFFKA
      220      230      240      250      260      270      280

      140      150      160      170      180      190      200
      SPSPIRTPrAVRPLRRRQ-----PKKSNELPQANRLPGIFDDVHGSHGRQVCRRHELYVSFQDLGWLDWVIA
      |  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      TEVHFRSIRSTGSKQRSQNRSKTPKNQEALRMAN-----VAENSSSDQRQACKKHLYVSFRDLGWQDWIIA
      290      300      310      320      330      340      350

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```

      210      220      230      240      250      260      270
PQGYSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPNVPAKACCAPTKLSATSVLYDSSNNVILRKHNRN
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
PEGYAAYYCEGECAPFLNSYMNATNHAIIVQTLVHFINPETVPKPCCAPTQLNAISVLYFDDSSNVILKKYRN
      360      370      380      390      400      410      420

      X
MVKKACGCH
| | | | | | |
MVKKACGCH
      430

```

1. US-07-800-364A-14 (1-281)

BMP7_HUMAN BONE MORPHOGENETIC PROTEIN 7 PRECURSOR (BMP-7) (OS

```

ID   BMP7_HUMAN      STANDARD;          PRT;   431 AA.
AC   P18075;
DT   01-NOV-1990 (REL. 16, CREATED)
DT   01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT   01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE   BONE MORPHOGENETIC PROTEIN 7 PRECURSOR (BMP-7) (OSTEOGENIC PROTEIN 1)
DE   (OP1).
GN   BMP7 OR OP1.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=PLACENTA;
RM   90291971
RA   OZKAYNAK E., RUEGER D.C., DRIER E.A., CORBETT C., RIDGE R.J.,
RA   SAMPATH T.K., OPPERMANN H.;
RL   EMBO J. 9:2085-2093(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RM   91088608
RA   CELESTE A.J., IANNAZZI J.A., TAYLOR R.C., HEWICK R.M., ROSEN V.,
RA   WANG E.A., WOZNEY J.M.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 87:9843-9847(1990).
CC   -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE
CC   OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF
CC   EPITHELIAL OSTEOGENESIS.
CC   -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC   -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR   EMBL; X51801; HSOP1.
DR   EMBL; M60316; HSTGFBD.
DR   PIR; S10529; S10529.
DR   PIR; C39263; C39263.
DR   PROSITE; PS00250; TGF_BETA.

```

KW SIGNAL; GROWTH FACTOR; CYTOKINE; BONE; CARTILAGE; GLYCOPROTEIN.
 FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 292 POTENTIAL.
 FT CHAIN 293 431 BONE MORPHOGENETIC PROTEIN 7.
 FT DISULFID 330 396 BY SIMILARITY.
 FT DISULFID 359 428 BY SIMILARITY.
 FT DISULFID 363 430 BY SIMILARITY.
 FT DISULFID 395 395 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 187 187 POTENTIAL.
 FT CARBOHYD 302 302 POTENTIAL.
 FT CARBOHYD 321 321 POTENTIAL.
 SQ SEQUENCE 431 AA; 49313 MW; 936534 CN;

Initial Score = 132 Optimized Score = 158 Significance = 54.74
 Residue Identity = 56% Matches = 161 Mismatches = 115
 Gaps = 11 Conservative Substitutions = 0

```

      X      10      20      30      40      50      60
      EPHWKEFRDLTQIPAGEAVTAAEFRIYK-VPSIHLNRTLHVSMFQVVQEQSNRESDLFFL
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
VEHDKEFFHPRYHHREFRDLSKIPEGEAVTAAEFRIYKDYIRERFDNETFRISVYQVLQEHLGRESDLFLL
140      150      160      170      180      190      200      210

      70      80      90      100      110      120      130
DLQTLRAGDEGLVLDVTAASDCWLLKRHKDLGLRLYVETEDGHSVDPGLAGLLGQRAPRSQQPFVVTFFRA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DSRTLWASEEGWLVFDITATSNHWVVNPRHNLGLQLSVETLDGQSINPKLAGLIGRHGFPQNKQPFMVAFFKA
220      230      240      250      260      270      280

140      150      160      170      180      190      200
SPSPIRTPRAVRPLRRRQ-----PKKSNELPQANRLPGIFDDVHGSHGRQVCRRHELYVSFQDLGWLDWVIA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
TEVHFRSIRSTGSKQRSQNRSKTPKNQEALRMAN-----VAENSSSDQRQACKKHELYVSFRDLGWQDWIIA
290      300      310      320      330      340      350

210      220      230      240      250      260      270
PQGYSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPNVAVPKACCAPTKLSATSVLYYDSSNNVILRKHRN
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
PEGYAAYYCEGECAPLNSYMNATNHAIQTLVHFINPETVPKPCCAPTQLNAISVLYFDDSSNVILKKYRN
360      370      380      390      400      410      420

      X
MVKKACGCH
| | | | |
MVRACGCH
430

```

2. US-07-800-364A-14 (1-281)

BMP7_MOUSE BONE MORPHOGENETIC PROTEIN 7 PRECURSOR (BMP-7) (OS

ID BMP7_MOUSE STANDARD; PRT; 430 AA.
 AC P23359;
 DT 01-NOV-1991 (REL. 20, CREATED)
 DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
 DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
 DE BONE MORPHOGENETIC PROTEIN 7 PRECURSOR (BMP-7) (OSTEOGENIC PROTEIN 1)
 DE (OP1).
 GN BMP7 OR OP1.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RM 91354237
 RA OZKAYNAK E., SCHNEGELSBERG P.N.J., OPPERMAN H.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 179:116-123(1991).
 CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE
 CC OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF
 CC EPITHELIAL OSTEOGENESIS.
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
 DR EMBL; X56906; MMOP1G.
 DR PIR; JQ1184; JQ1184.
 DR PROSITE; PS00250; TGF_BETA.
 KW SIGNAL; GROWTH FACTOR; CYTOKINE; BONE; CARTILAGE; GLYCOPROTEIN.
 FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 291 POTENTIAL.
 FT CHAIN 292 430 BONE MORPHOGENETIC PROTEIN 7.
 FT DISULFID 329 395 BY SIMILARITY.
 FT DISULFID 358 427 BY SIMILARITY.
 FT DISULFID 362 429 BY SIMILARITY.
 FT DISULFID 394 394 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 186 186 POTENTIAL.
 FT CARBOHYD 301 301 POTENTIAL.
 FT CARBOHYD 320 320 POTENTIAL.
 FT CARBOHYD 371 371 POTENTIAL.
 SQ SEQUENCE 430 AA; 49283 MW; 934349 CN;

Initial Score = 132 Optimized Score = 155 Significance = 53.32
 Residue Identity = 55% Matches = 158 Mismatches = 118
 Gaps = 11 Conservative Substitutions = 0

	X	10	20	30	40	50	60
	EPHWKEFRFDLTQIPAGEAVTAAEFRIYK-VPSIHLNRTLHVSMFQVVQE QSNRESDLFFL						
	I	IIIIII	IIIIIIIIII	II	IIII	IIIIII	I
140	150	160	170	180	190	200	210
	70	80	90	100	110	120	130
	DLQTLRAGDEGLVLDVTAASDCWLLKRHKDLGLRLYVETEDGHSVDPGLAGLLGQRAPRSQQPFVVTFFRA						

FT CHAIN 323 454 BONE MORPHOGENETIC PROTEIN 5.
 FT DISULFID 353 419 BY SIMILARITY.
 FT DISULFID 382 451 BY SIMILARITY.
 FT DISULFID 386 453 BY SIMILARITY.
 FT DISULFID 418 418 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 211 211 POTENTIAL.
 FT CARBOHYD 327 327 POTENTIAL.
 FT CARBOHYD 345 345 POTENTIAL.
 FT CARBOHYD 395 395 POTENTIAL.
 SQ SEQUENCE 454 AA; 51736 MW; 1034006 CN;

Initial Score = 111 Optimized Score = 153 Significance = 52.36
 Residue Identity = 54% Matches = 155 Mismatches = 125
 Gaps = 2 Conservative Substitutions = 0

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      X      10      20      30      40      50      60
      EPHWKEFRDLTQIPAGEAVTAAEFRIYKVPS-IHLLNRTLHVSMFQVVQEQSNRESDLFFL
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
VERDKDFSHQRRHYKEFRDLTQIPHGEAVTAAEFRIYKDRSNNRFENETIKISIIYQIIKEYTNRDADLFL
    170 X 180      190      200      210      220      230

      70      80      90      100     110     120     130
DLQTLRAGDEGWLVLVDVTAASDCWLLKRHKDLGLRLYVETEDGHSVDPGLAGLLGQRAPRSQQPFVVTFFRA
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DTRKAQALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRSINVKSAGLVGRQGPQSKQPFMVAFKFA
    240     250     260     270     280     290     300

      140     150     160     170     180     190     200
SPSPIRTFRAVRPLRRRQPKKSNELPQANRLPGIFDDVHGSHGRQVCCRHELYVSFQDLGWLDWVIAPQGYG
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
SEVLLRSVRA-ANKRKNQNRNKSSSHQDSSRMSSVGDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYA
    310     320     330     340     350     360     370

      210     220     230     240     250     260     270
AYYCEGECSFPLDSCMNATNHAILQSLVHLMKPNVPAKCAPTKLSATSVLYDSSNNVILRKHRNMVVKA
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
AFYCDGECSSFPLNAHMNATNHAI VQTLVHLMFPDHPKPCAPTKLNAISVLYFDDSSNVILKKYRNMVVRS
    380     390     400     410     420     430     440     450
  
```

280
 CGCH
 | | | |
 CGCH
 X

1/5/1 (Item 1 from file: 351)
008644667 WPI Acc No: 91-148697/20
XRAM Acc No: C91-064306

Osteogenic device for implantation in a mammal - comprising a matrix of treated collagen particles and a protein which induces bone formation

Patent Assignee: (CREA-) CREATIVE BIOMOLECULES INC; (CREA-) CREATIVE BIOMOLECUL

Author (Inventor): OPPERMAN H; KUBERASAMP T; RUEGER D C; OZKAYNAK E; PANG R H L

Number of Patents: 005

Number of Countries: 017

Patent Family:

CC Number	Kind	Date	Week	
WO 9105802	A	910502	9120	(Basic)
CA 2027259	A	910418	9126	
AU 9066481	A	910615	9133	
EP 448704	A	911002	9140	
JP 4502336	W	920423	9223	

Priority Data (CC No Date): US 422699 (891017); US 483913 (900222); US 569920 (900820)

Applications (CC, No, Date): JP 90515578 (901015); WO 90US5903 (901015); EP 90916655 (901015)

Language: English

EP and/or WO Cited Patents: EP 128041; EP 148155; EP 169001; EP 169016; EP 182483; EP 212474; EP 230647; EP 309241; US 4172128; US 4294753; US 4394370; US 4434094; US 4563350; US 4563489; US 4657548; US 4703108; US 4725671; US 4789663; US 4812120; US 4824939; US 4837285; US 4894441; WO 8600526; WO 8800205; WO 8909605; WO 8910409; 11Jnl.Ref

Designated States

(National): AU; CA; JP

(Regional): AT; BE; CH; DE; DK; ES; FR; GB; GR; IT; LU; NL; SE; LI

Filing Details: JP04502336 Based on WO 9105802

Abstract (Basic): WO 9105802

An osteogenic device for implantation in a mammal comprises (a) a biocompatible, in vivo biodegradable matrix of mineral-free, delipidated Type I insol. bone collagen particles, depleted in noncollagenous protein and (b) a protein (I) produced by the expression of recombinant DNA in a mammalian cell, (I) comprising 2 oxidised subunits, the amino acid sequence of each subunit being sufficiently duplicative of the amino acid sequence shown (OP1-16V) such that the dimeric species comprising the subunits has a conformation that is capable of inducing endochondral bone formation in a mammal when disposed within the matrix and implanted in the mammal.

An osteogenic protein expressed from recombinant DNA in a mammalian host cell and capable of inducing endochondral bone formation in a mammal when disposed within a matrix implanted in the mammal, comprises (I). Also claimed are a biocompatible, in vivo biodegradable matrix for implantation in a mammal, an osteogenic protein expressed from recombinant DNA in a mammalian host cell, and a biocompatible, in vivo biodegradable matrix for implantation.

USE/ADVANTAGE - The collagen particles are treated to increase the intraparticle porosity and the surface area of the particles. The matrix obtd. may be combined with osteogenic protein to induce endochondral bone formation reliably and reproducibly in a mammalian body. The osteogenic device can induce at the locus of the implant the full developmental cascade of endochondral bone formation including vascularisation, mineralisation and bone marrow differentiation. (I)

has bone-inducing activity which is highly reproducible and does

dependent. @ (105pp Dwg. No. 0/13) @

File Segment: CPI

Derwent Class: B07; D22;

Int Pat Class: A61K-037/02; A61K-037/12; C07K-015/06; C07K-017/02;

C09H-001/02; C12N-015/00

Chemical Fragment Codes (M1):

01 M423 M424 M710 M740 M903 N135 P421 P714 Q233 V752

Chemical Fragment Codes (M6):

02 M903 P421 P714 Q233 R220

?

1. US-07-800-364A-7 (1-199)
Q15242 BMP-8 peptide.

ID Q15242 standard; DNA; 199 BP.
AC Q15242;
DT 09-MAR-1992 (first entry)
DE BMP-8 peptide.
KW Cartilage; wound healing; tissue repair; BMP; ss.
OS Bos taurus.
FH Key Location/Qualifiers
FT CDS 30..176
FT /*tag= a
FT /label= BMP-8
PN W09118098-A.
PD 28-NOV-1991.
PF 15-MAY-1991; U03388.
PR 16-MAY-1990; US-525357.
PR 15-JAN-1991; US-641204.
PA (GENE-) GENETICS INST INC.
PI Hewick RM, Wang JH;
DR WPI; 91-369252/50.
DR P-PSDB; R15522.
PT New BMP-8 protein - useful in inducing cartilage and/or bone
PT formation to treat wounds and repair fractures and tissues, e.g.
PT burns, incisions and ulcers
PS Disclosure; Page 27; 50pp; English.
CC Nucleotide 95 is a "T" whereas in the amplified DNA fragment the
CC corresp. nucleotide is "C".
CC This sequence encodes amino acids 64-112 (C-terminal) of the BMP-8
CC sequence given in R15522. BMP-8 peptide fragments were purified from
CC ground bovine bone powder. Oligonucleotide probes were designed based
CC on these peptides and used to screen bovine genomic libraries to
CC isolate DNA sequences encoding BMP-8 proteins.
CC Pharmaceutical compsns. contg. BMP-8 can be used to aid bone and/or
CC cartilage formation or wound healing and tissue repair. The
CC proteins are not very species specific so can be used in domestic
CC and farm animals as well as humans.
CC See also Q15240-48, R15517 and R15522.
SQ Sequence 199 BP; 34 A; 87 C; 52 G; 26 T;

Initial Score = 199 Optimized Score = 199 Significance = 14.46
Residue Identity = 100% Matches = 199 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
TGCCCGCTGCCCCCTCCCGCCCCCGCCAGGTGCACCTGCTGAAGCCGCACGCGGTCCCCAAGGCGTGCTGCG
|||||
TGCCCGCTGCCCCCTCCCGCCCCCGCCAGGTGCACCTGCTGAAGCCGCACGCGGTCCCCAAGGCGTGCTGCG
X      10      20      30      40      50      60      70

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      80      90      100      110      120      130      140
CGCCCACCAAGCTGAGCGCCACTTCCGTGCTCTACTACGACAGCAGCAACAACGTCATCCTGCGCAAGCACC
|||||
CGCCCACCAAGCTGAGCGCCACTTCCGTGCTCTACTACGACAGCAGCAACAACGTCATCCTGCGCAAGCACC
      80      90      100      110      120      130      140

      150      160      170      180      190      X
GCAACATGGTGGTCCGCGCCTGCGGCTGCCACTGAGGCCCAACTCCACCGGCAG
|||||
GCAACATGGTGGTCCGCGCCTGCGGCTGCCACTGAGGCCCAACTCCACCGGCAG
      150      160      170      180      190      X

```

. US-07-800-364A-7 (1-199)

DR060APRO D.melanogaster 60A protein (60A) mRNA, complete cd

```

LOCUS      DR060APRO      1632 bp ss-mRNA      INV      11-SEP-1992
DEFINITION D.melanogaster 60A protein (60A) mRNA, complete cds.
ACCESSION  M84795
KEYWORDS   60A protein; bone morphogenetic protein;
           transforming growth factor.
SOURCE      Drosophila melanogaster (library: Kopczynski-Muskavitch) embryo
           cDNA to mRNA.
ORGANISM    Drosophila melanogaster
           Eukaryota; Animalia; Metazoa; Arthropoda; Uniramia; Insecta;
           Pterygota; Neoptera; Holometabola; Diptera; Brachycera;
           Cyclorrhapha; Schizophora; Drosophiloidea; Drosophilidae.
REFERENCE   1 (bases 1 to 1632)
AUTHORS     Doctor, J.S., Jackson, P.D., Rashka, K.E., Visalli, M. and
           Hoffmann, F.M.
TITLE       Sequence, biochemical characterization and developmental
expression  of a new member of the TGF-beta superfamily in Drosophila
           melanogaster
JOURNAL      Dev. Biol. 151, 491-505 (1992)
STANDARD     full automatic
FEATURES     Location/Qualifiers
CDS          142..1509
           /gene="60A"
           /product="60A protein"
           /codon_start=1

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/translation="MSGLRNTSEAVAVLASLGLGMVLLMFVATTPPAVEATQSGIYID

NGKDQTIMHRVLSDDKLDVSYEILEFLGIAERPTHLSSHQLSLRKSAPKFLLDVYHR

ITAEGLSDQDEDDDYERGHRSRRSADLEEDEGEQQKNFITDLKRAIDESDIIMTFL

NKRHHNVDEL RHEHGRRLWFDVSNVPNDNYLVMAELRIYQANEGKWL TANREFTITV

YAIGTGTLGQHTMEPLSSVNTTGDYVGWLELNVTEGLHEWLVKSKDNHGIYIGAHAVN
 RPDREVKLDDIGLIHRKVDDDEFQPFMIGFFRGPELIKATAHSSHRSKRSASHPRKRK
 KSVSPNNVPLLEPMESTRSCQMOTLYIDFKDLGWHDWIIAPEGYGAFYCSGECNFPLN
 AHMNATNHAIVQTLVHLLPEKKVPKPCCAPTRLGALPVLVHLNDENVNLKKYRNMIVK

SCGCH"

BASE COUNT 414 a 479 c 453 g 286 t
 ORIGIN chromosome 2R--60A

Initial Score = 104 Optimized Score = 123 Significance = 6.66
 Residue Identity = 63% Matches = 134 Mismatches = 62
 Gaps = 16 Conservative Substitutions = 0

```

      GACTTCAAGGATCTGGGCTGGCATGACTGGATCATCGCACCAGAGGGCTATGGCGCCTTCTACTGCAGCGGC
      1230      1240      1250      1260      1270      1280      1290

                                X          10          20          30
                                TGCCCGC--TGCCCCCTCC---CG-CCCCCGCCAGGTGCACCTG
                                || ||| | || || | || || | || ||| |||||
      GAGTGCAATTTCCCGCTCAATGCGCACATGAACGCCACGAACCATGCGATCGTCCAGACCCTGGTCCACCTG
      1300      1310      1320      X 1330      1340      1350      1360

      40          50          60          70          80          90          100
      CTGAAGCCGCACGCGGTCCCCAAGGCGTGCTGCGCGCCCAACCAAGCTGAGCGCCACT-TCCGTGCTCTACTA
      ||| ||||| | ||| ||||| | ||||| || |||| |||| | |||| |||| |||| |
      CTGGAGCCGAAGAAGGTGCCCAAGCCCTGCTGCGCTCCGACCAGGCTGGGAG-CACTACCCGTTCTGTACCA
      1370      1380      1390      1400      1410      1420      1430

      110         120         130         140         150         160         170         180
      CGACAGCAGCAACAACGTCATCCTGCGCAAGCACCGCACATGGTGGTCCGCGCCTGCGGCTGCCACTGAGG
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      CCTGAACGACGAGAATGTGAACCTGAAAAAGTATAGAAACATGATTGTGAAATCCTGCGGGTGCCATTGA--
      1440      1450      1460      1470      1480      1490      1500

                                190          X
                                CCCCCA--CCAC--CGGC--AG
                                ||| | |||| ||| ||
      ATTC AATTTACCACTTAGGCTAAGCACTATAGCACTATATATAAGCATTCTGTGTAGATGTCCATCTCTG
      1510      1520      1530      X 1540      1550      1560      1570      1580

      TACTAATCTCGAATATTTTTATACAAAATATACAGCGCTGTACCTAACTG
      1590      1600      1610      1620      1630
  
```

1. US-07-800-364A-7 (1-199)
 QQBE8 BPLF1 protein - Human herpesvirus 4 (strain B95-8)

ENTRY QQBE8 #Type Protein
 TITLE BPLF1 protein - Human herpesvirus 4 (strain B95-8)
 DATE 25-Feb-1985 #Sequence 25-Feb-1985 #Text 31-Mar-1992
 PLACEMENT 1934.0 1.0 1.0 1.0 1.0
 SOURCE human herpesvirus 4, Epstein-Barr virus
 ACCESSION A03747
 REFERENCE (Protein coding region)
 #Authors Baer R., Bankier A.T., Biggin M.D., Deininger P.L.,
 Farrell P.J., Gibson T.J., Hatfull G., Hudson
 G.S., Satchwell S.C., Seguin C., Tuffnell P.S.,
 Barrell B.G.
 #Journal Nature (1984) 310:207-211
 #Title DNA sequence and expression of the B95-8
 Epstein-Barr virus genome.
 #Reference-number A03794
 COMMENT The sequence was translated from the DNA sequence,
 which was obtained from GenBank, release 26.0.
 SUMMARY #Molecular-weight 337955 #Length 3149 #Checksum 7480
 SEQUENCE

Initial Score = 20 Optimized Score = 24 Significance = 5.31
 Residue Identity = 37% Matches = 29 Mismatches = 35
 Gaps = 14 Conservative Substitutions = 0
 Translation Frame= 1

```

AHVRVSTYAH DILQYVGAPGAQYTCVHLYFLPEAFETEDPRIFMLEHYGVYDFYEANGSGFDLVGPPELVSSD
 210      220      230      240      250      260      270

                                X          10          20          30
                                CPLP-----PPAPAR---CTCXSRTRSPRRAARPPSXAPLP
                                III          IIII          I   II   III IIII
GEAAGTPGADSSPPVMLPFERRIIPYNLRPLPSRSFTSDSFPA-ARYSPAKTNSPPSSPASAA-PASAAPAS
280      290      300      X 310      320      330      340

      40      50      60      X
CSTTTAATTS-SCASTATWWSAPAAATEAPTPPA
  II  I   III  IIII  I   II
AAFASAAPASAAFPASAAFPASAAFPASAAFPASSPPLFIPIPLGLHTPGVPAPSTPPRASSGAAPQTPKRKKGLG
350      360      370      380      390      400      410

KDSPHKKPTSGRRLPLSSTTDTEDDQLPRTHVPPHRPPSAARLPPPVIPIPHQSPPASPTPH
420      430      440      450      460      470      480

```

1. US-07-800-364A-7 (1-199)
 TEGU_EBV LARGE TEGUMENT PROTEIN.

ID TEGU_EBV STANDARD; PRT; 3149 AA.
 AC P03186;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
 DE LARGE TEGUMENT PROTEIN.
 GN BPLF1.
 OS EPSTEIN-BARR VIRUS (STRAIN B95-8).
 OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RM 84270667
 RA BAER R., BANKIER A.T., BIGGIN M.D., DEININGER P.L., FARRELL P.J.,
 RA GIBSON T.J., HATFULL G., HUDSON G.S., SATCHWELL S.C., SEGUIN C.,
 RA TUFFNELL P.S., BARRELL B.G.;
 RL NATURE 310:207-211(1984).
 CC -!- FUNCTION: TEGUMENT PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
 CC EBV BPLF1, AND VZV 22.
 DR EMBL; V01555; EBV.
 DR PIR; A03747; QQBE8.
 SQ SEQUENCE 3149 AA; 337954 MW; 1.650784E+07 CN;

Initial Score = 20 Optimized Score = 24 Significance = 5.70
 Residue Identity = 37% Matches = 29 Mismatches = 35
 Gaps = 14 Conservative Substitutions = 0
 Translation Frame= 1

```

AHVRVSTYAH DILQYVGAPGAQYTCVHLYFLPEAFETEDPRIFMLEHYGVYDFYEANGSGFDLVGP ELVSSD
 210      220      230      240      250      260      270

                                X          10          20          30
                                CPLP-----PPAPAR---CTCXSRTRSPRRAARPPSXAPLP
                                |||          || ||          |  ||  || || || ||
GEAAGTPGADSSPPVMLPFERRIIPYNLRPLPSRSFTSDSFPA-ARYSPAKTNSPPSSPASAA-PASAAPAS
280      290      300      X 310      320      330      340

      40      50      60      X
CSTTTAATTS-SCASTATWWSAPAAATEAPTPPA
  || |  || |  || |  |  ||
AAPASAAPASAAPASAAPASAAPASAAPASSPPLFIPIPGLGHTPGVPAPSTPPRASSGAAPQTFKRKKGLG
350      360      370      380      390      400      410

KDSPHKKPTSGRRLPLSSTTDTEDDQLPRTHVPPHRPPSAARLPPPVIPIPHQSPPASPTPH
420      430      440      450      460      470      480
  
```

2. US-07-800-364A-7 (1-199)
 Y115_ADE02 HYPOTHETICAL PROTEIN E-115.

ID Y115_ADE02 STANDARD; PRT; 115 AA.
AC P03290;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL PROTEIN E-115.
OS HUMAN ADENOVIRUS TYPE 2.
OC VIRIDAE; DS-DNA NONENVELOPED VIRUSES; ADENOVIRIDAE.
RN [1]
RP SEQUENCE FROM N.A.
RM 83056843
RA GINGERAS T.R., SCIAKY D., GELINAS R.E., BING-DONG J., YEN C.E.,
RA KELLY M.M., BULLOCK P.A., PARSONS B.L., O'NEILL K.E., ROBERTS R.J.;
RL J. BIOL. CHEM. 257:13475-13491(1982).
DR EMBL; J01917; AD2.
DR PIR; A03862; A03862.
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 115 AA; 12236 MW; 68893 CN;

Initial Score = 12 Optimized Score = 23 Significance = 5.18
Residue Identity = 29% Matches = 26 Mismatches = 40
Gaps = 21 Conservative Substitutions = 0
Translation Frame= 1

```

              X      10              20      30      40
              CPLPPAPARCTCXSRTRS-----PRRAARPPSXAPLPCSTTTAAT
              |  | | | | | | | | | | | | | | | | | | | |
MGETWFLTPNGQSSPGSWNARPSAGPAARMPTPRNRYFSRPSSTPLKVCTAPRAAPPPRASCAPRATPRRGW
          10      20      30      40      50      60      70

          50              60      X
          TSSCASTATW-----WSAPA-AATEAPTPPA
          |  | | | | | | | | | | | | | | | | | | | |
          TMTWPSNATWPTRRAKTGSASAPAGPASSAPWPAPSPERTPSP

```

1. US-07-800-364A-9 (1-172)

A33532 *Mucin - Human (fragment)

ENTRY A33532 #Type Protein (fragment)
TITLE *Mucin - Human (fragment)
DATE 04-Sep-1992 #Sequence 04-Sep-1992 #Text 04-Sep-1992
PLACEMENT 0.0 0.0 0.0 0.0 0.0
COMMENT *This entry is not verified.
SOURCE Homo sapiens #Common-name man
REFERENCE
#Authors Gum J.R., Byrd J.C., Hicks J.W., Toribara N.W.,
Lampert D.T.A., Kim Y.S.
#Journal J. Biol. Chem. (1989) 264:6480-6487

#Title Molecular cloning of human intestinal mucin cDNAs.
 Sequence analysis and evidence for genetic
 polymorphism.
 #Reference-number A33532
 #Accession A33532
 #Cross-reference GB:M22404; GB:M22405; GB:M22406
 SUMMARY #Length 519 #Checksum 4853
 SEQUENCE

Initial Score = 11 Optimized Score = 23 Significance = 7.36
 Residue Identity = 33% Matches = 26 Mismatches = 31
 Gaps = 20 Conservative Substitutions = 0
 Translation Frame= 1

1. US-07-800-364A-11 (1-119)

S16244 Bone morphogenetic protein 2 precursor - African

ENTRY S16244 #Type Protein
 TITLE Bone morphogenetic protein 2 precursor - African
 clawed frog
 DATE 30-Jun-1992 #Sequence 30-Jun-1992 #Text 31-Sep-1992
 PLACEMENT 0.0 0.0 0.0 0.0 0.0
 SOURCE Xenopus laevis #Common-name African clawed frog
 ACCESSION S16244
 REFERENCE
 #Authors Plessow S., Koester M., Knoechel W.
 #Journal Biochim. Biophys. Acta (1991) 1089:280-282
 #Title cDNA sequence of Xenopus laevis bone morphogenetic
 protein 2 (BMP-2).
 #Reference-number S16244
 #Accession S16244
 #Molecule-type mRNA
 #Residues 1-398 (PLE)
 #Cross-reference EMBL:X55031
 KEYWORDS dimer\ glycoprotein
 FEATURE
 285-398 #Protein bone morphogenetic protein 2
 (predicted) (MAT)\
 137,202,340 #Binding-site carbohydrate (Asn)
 (covalent) (predicted)
 SUMMARY #Molecular-weight 45575 #Length 398 #Checksum 9714
 SEQUENCE

Initial Score = 11 Optimized Score = 15 Significance = 6.02
 Residue Identity = 32% Matches = 18 Mismatches = 21
 Gaps = 16 Conservative Substitutions = 0
 Translation Frame= 1

```

SDSSKLHRINIYDIVKPAAASRGPVVRLLDTRLVHHNESKWESFDVTPAIARWIAHKQPNHGFVVEVNHL
170      180      190      200      210      220      230

X      10      20
PLRVPADD--VHGSHGRQ-----VCRRHLYVSFQ
      |      |      |      |      |      |      |      |
NDKNVPKKHVIRISRLTPDKDNWPQIRPLLVTFSHDGKGHALHKRQKRQARHKQRKRLKSSCRRHPLYVDFS
240      250      260      X 270      280      290      300

30      X
DLGWLVSDDSP
      |      |      |
DVGWNDWIVAPPGYHAFYCHGECFPFLADHLNSTNHAIIVQTLVNSVNTNIPKACCVPTELSAISMLYLDENE
310      320      330      340      350      360      370      380

KVVLKNYQDMVVEGCGCR
390

```

2. US-07-800-364A-11 (1-119)

B39263 *Bone morphogenetic protein 6 - Human

```

ENTRY      B39263      #Type Protein
TITLE      *Bone morphogenetic protein 6 - Human
DATE       04-Oct-1991 #Sequence 04-Oct-1991 #Text 04-Oct-1991
PLACEMENT      0.0      0.0      0.0      0.0      0.0
COMMENT      *This entry is not verified.
SOURCE      Homo sapiens #Common-name man
REFERENCE
  #Authors   Celeste A.J., Iannazzi J.A., Taylor R.C., Hewick
              R.M., Rosen V., Wang E.A., Wozney J.M.
  #Journal   Proc. Natl. Acad. Sci. U.S.A. (1990) 87:9843-9847
  #Title     Identification of transforming growth factor beta
              family members present in bone-inductive protein
              purified from bovine bone.
  #Reference-number A39263
  #Accession   B39263
  #Cross-reference GB:M38694
SUMMARY      #Molecular-weight 57225 #Length 513 #Checksum 183
SEQUENCE

```

```

Initial Score      =      14      Optimized Score      =      19      Significance      = 10.04
Residue Identity   =      50%      Matches              =      20      Mismatches      =      19
Gaps               =      1      Conservative Substitutions      =      0
Translation Frame=      1

```

```

DTRVVWASEEGWLEFDITATSNLWVVTPQHNMGQLQSVVTRDGVHVHPRAAGLVGRDGPYDKQPFMVAFK
300      310      320      330      340      350      360

X      10      20      30      X

```

```

                                PLRV-PADDVHGSHGRQVCRRHELIVSFQDLGWLVSDDSP
                                || | | | | | | | | | | | | | | | |
SEVHVRTTRSASSRRRQQSRNRSTQSQDVARVSSASDYNSSSELKTACRKHELIVSFQDLGWQDWIIAPKGYA
 370          380          390 X   400          410          420          430 X

ANYCDGECSFPLNAHMNATNHAIVQTLVHLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRA
440          450          460          470          480          490          500

CGCH
510

```

3. US-07-800-364A-11 (1-119)

JQ1184 Osteogenic protein 1 precursor - Mouse

```

ENTRY          JQ1184      #Type Protein
TITLE          Osteogenic protein 1 precursor - Mouse
DATE           31-Dec-1991 #Sequence 31-Dec-1991 #Text 31-Sep-1992
PLACEMENT      0.0    0.0    0.0    0.0    0.0
SOURCE         Mus musculus #Common-name house mouse
ACCESSION      JQ1184\ PQ0224
REFERENCE

```

```

#Authors      Oezkaynak E., Schnegelsberg P.N.J., Oppermann H.
#Journal      Biochem. Biophys. Res. Commun. (1991) 179:116-123
#Title        Murine osteogenic protein (OP-1): high levels of
               mRNA in kidney.

```

```

#Reference-number JQ1184
#Accession      JQ1184
#Molecule-type DNA
#Residues       1-120 (OEZ)
#Cross-reference EMBL:X56906
#Accession      PQ0224
#Molecule-type mRNA
#Residues       54-430 (OE2)

```

COMMENT This protein induces bone formation.

FEATURE

```

1-29           #Domain signal sequence (SIG)\
30-290         #Peptide propeptide (predicted) (PRO)\
291-430        #Protein osteogenic protein-1
               (experimental) (MAT)\
186,301,320,371 #Binding-site carbohydrate (Asn)
               (covalent) (predicted)

```

```

SUMMARY        #Molecular-weight 49283 #Length 430 #Checksum 9190
SEQUENCE

```

```

Initial Score   =    14   Optimized Score   =    17   Significance =   8.03
Residue Identity =   45%   Matches           =    18   Mismatches  =    21
Gaps            =     1   Conservative Substitutions =     0
Translation Frame=     1

```

```

DSRTIWASEEGWL VFDITATSNHWVVNPRHNLGLQLSVETLDGQSINPKLAGLIGRHGPQNKQPFMVAFKKA
      220      230      240      250      260      270      280
                        X      10      20      30      X
                        PLR-VPADDVHGSHGRQVCRRHELIVSFQDLGWLVSDDSP
                        ||      |  ||  |  |||||  ||||  |
TEVHLRSIRSTGGKQRSQNRSKTPKNQEALRMASVAENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYA
      290      300      310      320      330      340      350

AYYCEGECAPLNSYMNATNHAIVQTLVHFINPDTVPKPCCAPTQLNAISVLYFDDSSNVILKKYRNMVVRA
      360      370      380      390      400      410      420

CGCH
430

```

4. US-07-800-364A-11 (1-119)

C39263 *Bone morphogenetic protein 7 - Human

```

ENTRY      C39263      #Type Protein
TITLE      *Bone morphogenetic protein 7 - Human
DATE       04-Oct-1991 #Sequence 04-Oct-1991 #Text 04-Oct-1991
PLACEMENT      0.0      0.0      0.0      0.0      0.0
COMMENT      *This entry is not verified.
SOURCE      Homo sapiens #Common-name man
REFERENCE
  #Authors   Celeste A.J., Iannazzi J.A., Taylor R.C., Hewick
              R.M., Rosen V., Wang E.A., Wozney J.M.
  #Journal   Proc. Natl. Acad. Sci. U.S.A. (1990) 87:9843-9847
  #Title     Identification of transforming growth factor beta
              family members present in bone-inductive protein
              purified from bovine bone.
  #Reference-number A39263
  #Accession  C39263
  #Cross-reference GB:M38695
SUMMARY     #Molecular-weight 49313 #Length 431 #Checksum 128
SEQUENCE

```

```

Initial Score      =      14      Optimized Score      =      17      Significance      =      8.03
Residue Identity   =      45%      Matches              =      18      Mismatches      =      21
Gaps               =      1      Conservative Substitutions      =      0
Translation Frame=      1

```

```

DSRTLWASEEGWL VFDITATSNHWVVNPRHNLGLQLSVETLDGQSINPKLAGLIGRHGPQNKQPFMVAFKKA
      220      230      240      250      260      270      280
                        X      10      20      30      X
                        PLR-VPADDVHGSHGRQVCRRHELIVSFQDLGWLVSDDSP
                        ||      |  ||  |  |||||  ||||  |
TEVHFRSIRSTGSKQRSQNRSKTPKNQEALRMANVAENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYA

```

```

      290      300      310 X      320      330      340      350
A Y Y C E G E C A F P L N S Y M N A T N H A I V Q T L V H F I N P E T V P K P C C A P T Q L N A I S V L Y F D D S S N V I L K K Y R N M V V R A
      360      370      380      390      400      410      420

```

CGCH
430

5. US-07-800-364A-11 (1-119)

S10529 *Osteogenic protein precursor - Human

ENTRY S10529 #Type Protein
 TITLE *Osteogenic protein precursor - Human
 DATE 15-Jun-1992 #Sequence 15-Jun-1992 #Text 15-Jun-1992
 PLACEMENT 0.0 0.0 0.0 0.0 0.0
 COMMENT *This entry is not verified.
 SOURCE Homo sapiens #Common-name man
 REFERENCE

#Authors Ozekaynak E., Rueger D.C., Drier E.A., Corbett C.,
 Ridge R.J., Sampath T.K., Oppermann H.

#Journal EMBO J. (1990) 9:2085-2093

#Title OP-1 cDNA encodes an osteogenic protein in the
 TGF-beta family.

#Reference-number S10529

#Accession S10529

#Cross-reference EMBL:X51801

SUMMARY #Molecular-weight 49313 #Length 431 #Checksum 128

SEQUENCE

Initial Score = 14 Optimized Score = 17 Significance = 8.03
 Residue Identity = 45% Matches = 18 Mismatches = 21
 Gaps = 1 Conservative Substitutions = 0
 Translation Frame= 1

```

DSRTLWASEEGWL VFDITATSNHWVVNPRHNLGLQLSVETLDGQSINPKLAGLIGRHGFPQNKQPFMVAFKKA
      220      230      240      250      260      270      280

```

```

          X          10          20          30          X
          PLR-VPADDVHGSHGRQVCRRHELIVSFQDLGWLVSDDSP
          ||          |  ||  |  |||||  |||  |

```

```

TEVHFRSIRSTGSKQRSQNRSKTPKNQEALRMANVAENSSSDQRQACKKHELIVSFRDLGWQDWIIAPEGYA
      290      300      310 X      320      330      340      350

```

```

A Y Y C E G E C A F P L N S Y M N A T N H A I V Q T L V H F I N P E T V P K P C C A P T Q L N A I S V L Y F D D S S N V I L K K Y R N M V V R A
      360      370      380      390      400      410      420

```

CGCH
430

6. US-07-800-364A-11 (1-119)

A33925 *Vg-1-related protein precursor - Mouse

ENTRY A33925 #Type Protein
 TITLE *Vg-1-related protein precursor - Mouse
 DATE 19-Sep-1992 #Sequence 19-Sep-1992 #Text 19-Sep-1992
 PLACEMENT 0.0 0.0 0.0 0.0 0.0
 COMMENT *This entry is not verified.
 SOURCE Mus musculus #Common-name house mouse
 REFERENCE
 #Authors Lyons K., Graycar J.L., Lee A., Hashmi S., Lindquist
 P.B., Chen E.Y., Hogan B.L.M., Derynck R.
 #Journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:4554-4558
 #Title Vgr-1, a mammalian gene related to Xenopus Vg-1, is
 a member of the transforming growth factor
 beta-gene superfamily.
 #Reference-number A33925
 #Accession A33925
 #Cross-reference GB:J04566
 SUMMARY #Molecular-weight 48788 #Length 438 #Checksum 9769
 SEQUENCE

Initial Score = 15 Optimized Score = 17 Significance = 8.03
 Residue Identity = 43% Matches = 17 Mismatches = 22
 Gaps = 0 Conservative Substitutions = 0
 Translation Frame= 1

```

      TRVVWASEEGWLEFDITATSNLWVVTPQHNMGQLQSVVTRDGLHVNPRAGLVGRDGPYDKQPFMVAFKVS
220      230      240      250      260      270      280      290

                                X      10      20      30      X
                                PLRVPADDVHGSHGRQVCRRHELYVSFQDLGWLVSDDSP
                                |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
EVHVRTTRSASSRRRQQRNRSTQSQDVSRGSGSSDYNGSELKTACKKHELYVSFQDLGQDWIIAPKGYAA
      300      310      320      330      340      350      360

      NYCDGECFPLNAHMNATNHAIVQTLVHLMNPEYVVPKPCCAPTKLNAISVLVYDDNSNVILKKYRNMVVRAC
      370      380      390      400      410      420      430

      GCH
  
```

7. US-07-800-364A-11 (1-119)

A39263 *Bone morphogenetic protein 5 - Human

ENTRY A39263 #Type Protein
 TITLE *Bone morphogenetic protein 5 - Human
 DATE 04-Oct-1991 #Sequence 04-Oct-1991 #Text 04-Oct-1991
 PLACEMENT 0.0 0.0 0.0 0.0 0.0

COMMENT *This entry is not verified.
 SOURCE Homo sapiens #Common-name man
 REFERENCE
 #Authors Celeste A.J., Iannazzi J.A., Taylor R.C., Hewick
 R.M., Rosen V., Wang E.A., Wozney J.M.
 #Journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:9843-9847
 #Title Identification of transforming growth factor beta
 family members present in bone-inductive protein
 purified from bovine bone.
 #Reference-number A39263
 #Accession A39263
 #Cross-reference GB:M38693
 SUMMARY #Molecular-weight 51736 #Length 454 #Checksum 4416
 SEQUENCE

Initial Score = 11 Optimized Score = 16 Significance = 7.03
 Residue Identity = 41% Matches = 16 Mismatches = 23
 Gaps = 0 Conservative Substitutions = 0
 Translation Frame= 1

```

DTRKAQALDVGLVFDITVTSNHVWINPQNNLGLQLCAETGDGRSINVKSAGLVGRQGPQSKQPFMVAFKKA
 240      250      260      270      280      290      300

                        X      10      20      30      X
                        PLRVPADDVHGSHGRQVCRRHELIVSFQDLGWLVSDDSP
                        |  |  |  |  |  |  |  |  |  |  |  |  |
SEVLLRSVRAANKRKNQNRNKSSSHQDSSRMSSVGDYNTSEQKQACKKHELIVSFRDLGWQDWIIAPEGYAA
310      320      330      X 340      350      360      370      X
FYCDGECFPLNAHMNATNHAIVQTLVHLMFPDHVPKPCCAPTKLNAISVLVYFDDSSNVILKKYRNMVVRSC
380      390      400      410      420      430      440      450

GCH

```

8. US-07-800-364A-11 (1-119)

C39364 *GDF-1 embryonic growth factor - Human

ENTRY C39364 #Type Protein
 TITLE *GDF-1 embryonic growth factor - Human
 DATE 03-Mar-1992 #Sequence 03-Mar-1992 #Text 03-Mar-1992
 PLACEMENT 0.0 0.0 0.0 0.0 0.0
 COMMENT *This entry is not verified.
 SOURCE Homo sapiens #Common-name man
 REFERENCE
 #Authors Lee S.J.
 #Journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:4250-4254
 #Title Expression of growth/differentiation factor 1 in the
 nervous system: conservation of a bicistronic

structure.
 #Reference-number A39364
 #Accession C39364

1. US-07-800-364A-11 (1-119)
 BMP6_HUMAN BONE MORPHOGENETIC PROTEIN 6 PRECURSOR (BMP-6).

ID BMP6_HUMAN STANDARD; PRT; 513 AA.
 AC P22004;
 DT 01-AUG-1991 (REL. 19, CREATED)
 DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
 DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
 DE BONE MORPHOGENETIC PROTEIN 6 PRECURSOR (BMP-6).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BONE;
 RM 91088608
 RA CELESTE A.J., IANNAZZI J.A., TAYLOR R.C., HEWICK R.M., ROSEN V.,
 RA WANG E.A., WOZNEY J.M.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 87:9843-9847(1990).
 CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
 CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
 DR EMBL; M60315; HSTGFBC.
 DR PIR; B39263; B39263.
 DR PROSITE; PS00250; TGF_BETA.
 KW SIGNAL; GROWTH FACTOR; CYTOKINE; BONE; CARTILAGE; GLYCOPROTEIN.
 FT SIGNAL 1 ? POTENTIAL.
 FT PROPEP ? 381 POTENTIAL.
 FT CHAIN 382 513 BONE MORPHOGENETIC PROTEIN 6.
 FT DISULFID 412 478 BY SIMILARITY.
 FT DISULFID 441 510 BY SIMILARITY.
 FT DISULFID 445 512 BY SIMILARITY.
 FT DISULFID 477 477 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 241 241 POTENTIAL.
 FT CARBOHYD 269 269 POTENTIAL.
 FT CARBOHYD 386 386 POTENTIAL.
 FT CARBOHYD 404 404 POTENTIAL.
 FT CARBOHYD 454 454 POTENTIAL.
 SQ SEQUENCE 513 AA; 57225 MW; 1340230 CN;

Initial Score = 14 Optimized Score = 19 Significance = 10.01
 Residue Identity = 50% Matches = 20 Mismatches = 19
 Gaps = 1 Conservative Substitutions = 0
 Translation Frame= 1

DTRVVWASEEGWLEFDITATSNLWVVTPQHNMGQLQLSVVTRDGVHVHPRAAGLVGRDGPYDKQPFMVAFKVV

```

      300      310      320      330      340      350      360
                X          10          20          30          X
                PLRV-PADDVHGSHGRQVCRRHELYVSFQDLGWLVSDDSP
                || || | | || ||||| ||||| |
SEVHVRTTRSASSRRRQQSRNRSTQSQDVARVSSASDYNSSSELKTACRKHELYVSFQDLGWQDWIIAPKGYA
      370      380      390      X      400      410      420      430      X

      ANYCDGECFPLNAHMNATNHAIVQTLVHLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRA
      440      450      460      470      480      490      500

```

CGCH
510

2. US-07-800-364A-11 (1-119)

BMP7_MOUSE BONE MORPHOGENETIC PROTEIN 7 PRECURSOR (BMP-7) (OS

```

ID  BMP7_MOUSE      STANDARD;      PRT;      430 AA.
AC  P23359;
DT  01-NOV-1991 (REL. 20, CREATED)
DT  01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT  01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE  BONE MORPHOGENETIC PROTEIN 7 PRECURSOR (BMP-7) (OSTEOGENIC PROTEIN 1)
DE  (OP1).
GN  BMP7 OR OP1.
OS  MUS MUSCULUS (MOUSE).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC  EUTHERIA; RODENTIA.
RN  [1]
RP  SEQUENCE FROM N.A.
RM  91354237
RA  OZKAYNAK E., SCHNEGELSBERG P.N.J., OPPERMANN H.;
RL  BIOCHEM. BIOPHYS. RES. COMMUN. 179:116-123(1991).
CC  -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE
CC  OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF
CC  EPITHELIAL OSTEOGENESIS.
CC  -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC  -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR  EMBL; X56906; MMOP1G.
DR  PIR; JQ1184; JQ1184.
DR  PROSITE; PS00250; TGF_BETA.
KW  SIGNAL; GROWTH FACTOR; CYTOKINE; BONE; CARTILAGE; GLYCOPROTEIN.
FT  SIGNAL          1      29      POTENTIAL.
FT  PROPEP          30     291      POTENTIAL.
FT  CHAIN           292     430      BONE MORPHOGENETIC PROTEIN 7.
FT  DISULFID        329     395      BY SIMILARITY.
FT  DISULFID        358     427      BY SIMILARITY.
FT  DISULFID        362     429      BY SIMILARITY.
FT  DISULFID        394     394      INTERCHAIN (BY SIMILARITY).

```

FT	CARBOHYD	186	186	POTENTIAL.
FT	CARBOHYD	301	301	POTENTIAL.
FT	CARBOHYD	320	320	POTENTIAL.
FT	CARBOHYD	371	371	POTENTIAL.
SQ	SEQUENCE	430 AA;	49283 MW;	934349 CN;

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Initial Score      =      14  Optimized Score =      17  Significance =  8.01
Residue Identity  =     45%  Matches           =      18  Mismatches    =     21
Gaps              =        1  Conservative Substitutions =        0
Translation Frame =        1
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DSRTIWASEEGWLVDITATSNHWVVNPRHNLGLQLSVETLDGQSI NPKLAGLIGRHGPQNKQPFMVAFKKA

X 10 20 30 X
PLR-VPADDVHGSHGRQVCRRHELYVSFQDLGWLVSDDSP

TEVHLRSIRSTGGKQRSGNRSKTPKNQEALRMASVAENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYA
290 300 310 320 330 340 350

AYYCEGECAPFLNSYMNATHAIVQTLVHFINPDTVPKPCCAPTQLNAISVLVFDDSSNVILKKYRNMVVRA
 360 370 380 390 400 410 420

CGCH
430

Set	Items	Description
?B 357,	155,	WPI, 72, 35, 5, 399

22jan93 15:09:16 User208701 Session D213.1
 \$0.14 0.004 Hrs File1
 \$0.14 Estimated cost File1
 \$0.04 DIALNET
 \$0.18 Estimated cost this search
 \$0.18 Estimated total session cost 0.004 Hrs.

SYSTEM:OS - DIALOG OneSearch

File 357:DERWENT BIOTECHNOLOGY ABS 1982-1992/DEC
 (Copr. 1993 Derwent Pub. Ltd.)
 File 155:MEDLINE 1966-1993/MAR (9303W3)
 File 351:DERWENT WORLD PATENTS INDEX-LATEST
 1981+;DW=9248,UA=9235,UM=9208
 **FILE351: Format 9 includes the expanded patent table. Preformatted
 REPORTs are available. Type ?FMT351, ?NEWS351, ?RATES351 for more info.
 File 350:Derwent World Patents Index
 1963-1980, EQUIVALENTS THRU DW=9243
 **FILE350: Format 9 includes the expanded patent table. Preformatted
 REPORTs are available. Type ?FMT350, ?NEWS350, ?RATES350 for more info.
 File 72:EMBASE (EXCERPTA MEDICA) 85-93/ISS02
 (COPR. ESP BV/EM 1993)
 **FILE 72: Truncate EMTREE Codes (e.g. DC=C1.120?) for complete
 **retrieval. The 9245 update has been delayed.
 File 35:DISSERTATION ABSTRACTS ONLINE 1861-FEB 93
 (Copr University Microfilms)
 File 5:BIOSIS PREVIEWS 69-93/JAN BA9503:BARRM4403
 (C. BIOSIS 1993)
 **FILE 5: Biosystematic Codes (BC=) for viruses have changed for 1993.
 Type ?NEWS5 for more information and a complete list of the new codes.
 File 399:CA SEARCH 1967-1992 UD=11726
 (COPR. 1993 BY THE AMER. CHEM. SOC.)
 **FILE399: Use is subject to the terms of your user customer agreement.

Set	Items	Description
?S HOP2?		AND OSTEOGENIC

2 HOP2?
 6400 OSTEOGENIC
 S1 0 HOP2? AND OSTEOGENIC
 ?s Glu(2W)pro(2W)his(2W)trp(2W)lys(2W)glu(2W)phe

Processing

20137 GLU
 77393 PRO
 133357 HIS
 15560 TRP
 22216 LYS
 20137 GLU
 26919 PHE
 S2 0 GLU(2W)PRO(2W)HIS(2W)TRP(2W)LYS(2W)GLU(2W)PHE
 ?s thr(2W)asn(2W)glu(2W)leu(2W)pro(2W)pro(2W)pro(2W)asn

\$4.77 Estimated cost File350
 \$1.58 0.008 Hrs File350
 \$1.58 Estimated cost File350
 \$6.26 0.058 Hrs File72
 \$6.26 Estimated cost File72
 \$2.21 0.023 Hrs File35
 \$2.21 Estimated cost File35
 \$2.40 0.025 Hrs File5
 \$2.40 Estimated cost File5
 \$5.17 0.041 Hrs File399
 \$5.17 Estimated cost File399
 OneSearch, 8 files, 0.200 Hrs File05
 \$2.16 DIALNET
 \$26.42 Estimated cost this search
 \$26.60 Estimated total session cost 0.204 Hrs.
 Logoff: level 29.01.08 D 15:20:53

DIALNET: call cleared by request

Enter Service:

please see your representative

if you are having trouble logging in??lx9~%104f

NO CARRIER

14167 THR
10800 ASN
20137 GLU
37663 LEU
77393 PRO
77393 PRO
77393 PRO
10800 ASN

S3 1 THR(2W)ASN(2W)GLU(2W)LEU(2W)PRO(2W)PRO(2W)PRO(2W)ASN
?T 3/5/1

3/5/1 (Item 1 from file: 351)
008865227 WPI Acc No: 91-369252/50
XRAM Acc No: C91-159207

New BMP-8 protein - useful in inducing cartilage and/or bone formation
to treat wounds and repair fractures and tissues, e.g. burns, incisions
and ulcers

Patent Assignee: (GENE-) GENETICS INST INC
Author (Inventor): HEWICK R M; WANG J H
Number of Patents: 001
Number of Countries: 014
Patent Family:

CC Number	Kind	Date	Week	
WO 9118098	A	911128	9150	(Basic)

Priority Data (CC No Date): US 525357 (900516); US 641204 (910115)

Language: English

EP and/or WO Cited Patents: 1.Jnl.Ref; WO 8910409; WO 9011366

Designated States

(National): CH; JP

(Regional): AT; BE; CH; DE; DK; ES; FR; GB; GR; IT; LU; NL; SE

Abstract (Basic): WO 9118098

A purified BMP-8 protein is claimed, comprising at least one of
the following sequences; (a)
Arg-His-Glu-Leu-Tyr-Val-Ser-Phe-Glu-Asp-Leu-Gly-Trp-Leu-Asp-Trp-Val-Ile
-Ala-Pro-Glu- Gly-Tyr; (b) Leu-Ser-Ala-Thr-Ser-Val-Leu
Tyr-Tyr-Asp-Ser-Ser-Asn-Asn-Val-Ile-Leu-Arg; (c)
Ala-Cys-Cys-Ala-Pro-Thr-Lys; (d) Thr-Asn-Glu-Leu-Pro-Pro-Pro
Asn-Lys-Leu-Pro-Gly-Ile-Phe-Asp-Asp-Val-His-Gly-Ser- His-Gly-Arg; and
(e) the sequences homologous to the above sequences. Also claimed are a
DNA sequence encoding a BMP-8 protein, a host cell transformed with the
DNA and a method for producing the protein.

USE/ADVANTAGE - BMP-8 protein induces the formation of cartilage
and/or bone and is used to heal wounds and repair tissue (claimed), eg
burns, incisions and ulcers. It is also used to repair fractures and
other defects or periodontal diseases. @ (50pp Dwg.No.0/0)@

File Segment: CPI

Derwent Class: B04; D16;

Int Pat Class: A61K-037/02; C12N-015/12; C12P-021/02

Manual Codes (CPI/A-N): B04-B04A; B04-B04A1; B04-C01; B12-A07; B12-J08;
B12-L02; B12-L03; D05-C12; D05-H03B; D05-H12

Chemical Fragment Codes (M1):

01 M423 M710 M903 P714 P738 P923 P941 P942 P943 Q233 V752 V753 V754

? PLEASE ENTER A COMMAND OR BE LOGGED OFF IN 5 MINUTES

?LOGOFF

22jan93 15:20:52 User208701 Session D213.2

\$1.24 0.008 Hrs File357

\$1.24 Estimated cost File357

\$0.63 0.019 Hrs File155

\$0.63 Estimated cost File155

\$2.97 0.015 Hrs File351

\$1.80 1 Type(s) in Format 5

\$1.80 1 Types

1. 5,011,691 , Apr. 30, 1991, Osteogenic devices; Hermann Oppermann, et al., 424/423, 426; 514/2, 21; 530/350, 395, 840 [IMAGE AVAILABLE]

US PAT NO: 5,011,691 [IMAGE AVAILABLE] L1: 1 of 1
DATE FILED: Feb. 23, 1989
REL-US-DATA: Continuation-in-part of Ser. No. 232,630, Aug. 15, 1988,
which is a continuation-in-part of Ser. No. 179,406,
Apr. 8, 1988, Pat. No. 4,968,590.

ABSTRACT:

Disclosed are (1) osteogenic devices comprising a matrix containing osteogenic protein and methods of inducing endochondral bone growth in mammals using the devices; (2) amino acid sequence data, amino acid composition, solubility properties, structural features, homologies and various other data characterizing osteogenic proteins, (3) methods of producing osteogenic proteins using recombinant DNA technology, and (4) osteogenically and chondroglucosaminoglycan active synthetic protein constructs.

#1691pn=s pn5=01165901

L1 1 PN=5011691

el,dbcitd, fcdi,tr,efld,,arb

1. 5,011,691 , Apr. 30, 1991, Osteogenic devices; Hermann Oppermann, et al., 424/423, 426; 514/2, 21; 530/350, 395, 840 [IMAGE AVAILABLE]

US PAT NO: 5,011,691 [IMAGE AVAILABLE] L1: 1 of 1
DATE FILED: Feb. 23, 1989
REL-US-DATA: Continuation-in-part of Ser. No. 232,630, Aug. 15, 1988,
which is a continuation-in-part of Ser. No. 179,406,
Apr. 8, 1988, Pat. No. 4,968,590.

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=> s Glu(2GW1)up(r2oW()2prWo)(h2isW()2hWi)st(r2pW()2tWr)p1(y2sW()2lWy)sg(12uW(W2gWb)up(h2e

L2 (2966)GLU

L3 (9856)PRO

L4 (107016)HIS

L5 (2510)TRP

L6 (2973)LYS

L7 (2966)GLU

L8 (3474)PHE

L9 0 GLU(2W)PRO(2W)HIS(2W)TRP(2W)LYS(2W)GLU(2W)PHE

=> s alas(2aW1)ac(y2sW)(c2yWs)c(y2sW()2cWy)sa(12aW()2aW1)ap(r2oW()2pWr)ot(h2rW(W2tWb)rl(y2s

L10 (3842)ALA

L11 (1903)CYS

L12 (1903)CYS

L13 (3842)ALA

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731
  cgtacatgcc
    ggccgtcaag
      gacggcgagt
        tcggcttcaa
          ccttctggtg

801
  ggcgggttca
    tcagcccca
      gaggtgggcc
        gaggcgttgc
          cgctcgacgc

851
  ctgggtcgcc
    ggggacgacg
      tcgtccccgt
        gtgcaaggcc
          atcctcgagg

901
  cgtaccggga. . .

```

EOGL06 Y

U.S. Patent & Trademark Office LOGOFF AT 14:28:29 ON 22 JAN 93

L14 (9836) PRO
 L15 (3202) THR
 L16 (2973) LYS
 L17 0 ALA(2W)CYS(2W)CYS(2W)ALA(2W)PRO(2W)THR(2W)LYS

=> s thrs(2tWh)ra(s2nW()2aWs)ng(12uW()2gW1)u1(e2uW()21We)up(r2oW()2pWr)op(r2oW)Wp2aWo)p(r2oW()2pWr)oa(s2n

L18 (3202) THR
 L19 (2046) ASN
 L20 (2966) GLU
 L21 (3565) LEU
 L22 (9856) PRO
 L23 (9856) PRO
 L24 (9856) PRO
 L25 (2046) ASN
 L26 0 THR(2W)ASN(2W)GLU(2W)LEU(2W)PRO(2W)PRO(2W)PRO(2W)ASN

#CCG??GAsA T?TGCACAGT?
 L27 23 ?GAATTC CG?

BCCB?L27S ALN2D7 ?AANDG C?CACCGAC?
 L28 (5)?AGCCCCA?
 L29 1 L27 AND ?AGCCCCA?

EL,ABCITD, FCIDT,,RFELD,,ARB

1. 4,997,930, Mar. 5, 1991, Cloning of complementary DNA encoding maize nitrite reductase; Kristine N. Lahners, et al., 536/27; 435/69.1, 70.1, 172.3, 240.4, 317.1, 320.1; 935/18, 21, 35, 64, 78, 79 [IMAGE AVAILABLE]

US PAT NO: 4,997,930 [IMAGE AVAILABLE] L29: 1 of 1
 DATE FILED: Mar. 16, 1989

ABSTRACT:

Maize cDNA coding for nitrite reductase is cloned, using a spinach nitrite reductase cDNA as a heterologous probe, and is characterized. A method is provided to use the cloned maize nitrite reductase cDNA to determine the number of nitrite reductase genes per maize genome and to study nitrite reductase mRNA regulation in maize.

=KWDCKWIDC

US PAT NO: 4,997,930 [IMAGE AVAILABLE] L29: 1 of 1

CLAIMS:

CLMS(2)

2. An isolated DNA sequence according to claim 1, wherein the sequence comprises:

1 gaattccggg
 ccgcacaggg
 cgcgcccgcg
 cggccgtctc
 cgtgccgccc
 51 ccggcggggg
 agcagggtccc
 gacggagcgg
 ctggagccga
 gggtcgagga
 101
 . . . tgtacgagca
 ccgcacatc
 aacgacctcg

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